

Table 10 shows sequence alignment between a NOV3 polypeptide with various fibromodulins: ACC NO: O43408 (SEQ ID NO:61), ACC NO: AP000597 (SEQ ID NO:7), ACC NO: O43155 (SEQ ID NO:62), ACC NO: O42235 (SEQ ID NO:63) and FMOD Bovin FM (SEQ ID NO:64). (Black outlined amino acids indicate potential regions of conserved sequence; greyed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs)

Insert the sequence listing pages 1 - 42 at the end of the specification.

#### **REMARKS**

The specification has been amended throughout to insert SEQ ID NO:34 – SEQ ID NO:64 which were omitted by typographical error and to insert the sequence listing. Applicants submit that the above amendments add no new matter.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned “**Version with markings to show changes made.**”

Applicants believe that no fee is due with the submission of this Preliminary Amendment. However, the Commissioner is hereby authorized to charge any additional fees that may be due, or credit any overpayment of same, to Deposit Account No. 50-0311, Attorney Reference No. 15966-585A (Cura-85A).

#### **CONCLUSION**

On the basis of the foregoing amendment and remark, Applicants respectfully submit that the pending claims are in condition for allowance. Should any questions or issues arise

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concerning this application, the Examiner is encouraged to contact the undersigned at the telephone number provided below.

Respectfully submitted,

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## Version with markings to show changes made

### **In the Specification:**

Table 2 on page 9 has been amended as follows:

**Table 2.**

## Comparison between a NOV1 polypeptide and thymosin beta-10 from human

>gb|AAA36746.1| (M92383) thymosin beta-10 [Homo sapiens]  
Length = 49

Score = 84.5 bits (192), Expect = 3e-16  
Identities = 34/40 (85%), Positives = 36/40 (90%), Gaps = 1/40 (2%)

NOV1 : 1 MADKPDIGEIASFNKAKLKKTEMQE-NTLLTKEAIEQEKR 39 (SEQ ID NO:2)  
||||||+|||||+|||||+|||||+|||||+|||||+|||||  
Sbjct: 6 MADKPDIGEIASFDKAKLKKTETQEKNLPTKETIEQEKR 45 (SEQ ID NO:34)

Table 3 on page 9 has been amended as follows:

Table 3.

## Multiple Sequence alignment of a NOV1 polypeptide and the thymosin beta family

(Black outlined amino acids indicate potential regions of conserved sequence; grayed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs.

Sequences may be referenced by the SWISSPROT or TREMBL ID.)

	10	20	30	40
thymosin beta family motif	.....	.....	.....	.....
NOV1 (2-38)	.....	.....	KLKKTETQE	N
TYB0_HUMAN (1-38)	ADKPD	GEIASFN	K	KLKKTETQE
TYB9_BOVIN (1-40)	ADKPD	GEIASFDK	A	N
TYB9_PIG (1-40)	ADKPD	GEINSFDK	A	KLKKTETQE
TYB4_HUMAN (1-40)	ADKPD	GEINSFDK	A	K
TYB4_MOUSE (7-47)	SDKPD	MAEIEKF	D	KLKKTETQE
TYB4_RABBIT (1-40)	SDKPD	MAEIEKF	D	K
TYB4_XENLA (1-39)	SDKPD	MAEIEKF	D	KLKKTETQE
TYBY_HUMAN (1-40)	SDKPD	MAEIEKF	D	K
TYBA_ONCMY (1-40)	SDKPD	MAEIEEV	A	KLKKTETQE
TYBB_ONCMY (1-40)	SDKPD	MAEIEEV	A	K
TYBB_LATJA (1-40)	SDKPD	MAEIEEV	A	KLKKTETQE
P97563_RAT (1-39)	MSDKPD	MAEIEEV	S	K
TYBN_HUMAN (1-38)	MSDKPD	MAEIEEV	S	KLKKTETQE
O97428_DROME (95-129)	MSDKPD	MAEIEEV	S	K
O97428_DROME (59-89)	MSDKPD	MAEIEEV	S	KLKKTETQE

Table 4 on page 10 has been amended as follows:

**Table 4.****PFAM alignment of a NOV1 polypeptide to the consensus sequence of the thymosin beta family**

>PD005116 (Closest domain: TYB0\_HUMAN 1-38)  
 Number of sequences in family: 16  
 Most frequent protein names: TYB4(4) TYB9(2) TYBB(2)  
 Commentary (automatic):  
     THYMOSIN ACETYLATION T-CELL DIFFERENTIATION  
     IMMUNOPOTENTIATION THYMUS BETA-4 ACTIN-BINDING PROTEIN  
     BETA  
     Length = 38  
     Score = 145 (60.9 bits), Expect = 5e-10  
     Identities = 32/38 (84%), Positives = 34/38 (89%), Gaps = 1/38 (2%)  
 NOV1:       2 ADKPDIGEIASFNKAALKKTEMQE-NTLLTKEAIEQEK 38 (SEQ ID NO:2)  
               |||||+|||||+||||||| ||| ||| |||||  
 Sbjct:       1 ADKPDIGEIASFDKAALKKTETQEKNLPTKETIEQEK 38 (SEQ ID NO:51)

Table 6 beginning on page 13 has been amended as follows:

**Table 6.****Comparison between a NOV2 polypeptide and mouse ephrin type-A receptor 8 precursor**

>ref|NP\_031965.1| Eph receptor A8  
 sp|O09127|EPA8\_MOUSE EPHRIN TYPE-A RECEPTOR 8 PRECURSOR (TYROSINE-PROTEIN KINASE  
 RECEPTOR EEK) (EPH-AND ELK-RELATED KINASE)  
 gb|AAB39218.1| (U72207) Eph-and Elk-related kinase [Mus musculus]  
 Length = 1004  
 Score = 3036 bits (7128), Expect = 0.0  
 Identities = 945/992 (95%), Positives = 964/992 (96%), Gaps = 1/992 (0%)  
 NOV2:  1 MAPARGRLLPPALWVVTAAAAAATCVSAARGEVNLLDTSTIHGDWGWLTPAHGWDSINEV 60  
       ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
 Sbjct: 1 MAPARARLSPALWVVTAAAAA-TCVSAGRGEVNLLDTSTIHGDWGWLTPAHGWDSINEV 59  
 NOV2:  61 DESFQPIHTYQVCNVMSPNQNNWLRTSWVPRDGARRVYAEIKFTLRLDCNSMPGVILGTCKE 120  
       |||||+||||| ||| ||| ||| |||+||||| ||| ||| ||| |||+||||| ||| |||  
 Sbjct: 60 DESFRPIHTYQVCNVMSPNQNNWLRTNWVPRDGARRVYAEIKFTLRLDCNSIPGVILGTCKE 119  
 NOV2: 121 TFNLYYLESDRDLGASTQESQFLKIDTIAADESFTGADLGVRLKLNTEVRSVGPLSKRG 180  
       |||||+||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
 Sbjct: 120 TFNLHYLESDRDLGASTQESQFLKIDTIAADESFTGADLGVRLKLNTEVRGVGVGPLSKRG 179  
 NOV2: 181 FYLAQDIGHACLAILSLRIYYKKCPAMVRNLAAFSEAVTGADESSSLVEVRGQCVRHSEER 240  
       ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
 Sbjct: 180 FYLAQDIGHACLAILSLRIYYKKCPAMVRNLAAFSEAVTGADESSSLVEVRGQCVRHSEER 239  
 NOV2: 241 DTPKMYCSAEGEWLVPIGKCVCSAGYEERRDACVACELGFYKSAPGDQLCARCPHSHSA 300  
       ||||| ||| ||| ||| ||| ||| ||| ||| |||+||||| ||| ||| |||  
 Sbjct: 240 DTPKMYCSAEGEWLVPIGKCVCSAGYEERRDACMACELGFYKSAPGDQLCARCPHSHSA 299  
 NOV2: 301 APAAQACHCDLSYYRAALDPPSACTRPPSAPVNLISSVNGTSVTLEWAPPPLDPGGRSDI 360  
       ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
 Sbjct: 300 TPAAQTCRCDLSYYRAALDPPSACTRPPSAPVNLISSVNGTSVTLEWAPPPLDPGGRSDI 359  
 NOV2: 361 TYNACRRCPWALSRCACSGTRFVPPQQTSLVQASLLVANLLAHMNYSFWIEAVNGVSD 420  
       ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||+|

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Sbjct: 360 TYNAVCRRCPWALSHCEACGSGTRFVPPQTSLAQASLLVANLLAHMNYSFWIEAVNGVSN 419  
NOV2: 421 LSPEPRRAAVNITTNAAPSQVVIRQERAGQTSVSLWQEPEQPNGIILEYEIKYYEK 480  
Sbjct: 420 LSPEPRSAAVNITTNAAPSQVVIRQERAGQTSVSLWQEPEQPNGIILEYEIKYYEK 479  
NOV2: 481 DKEMQSYSTLKVATTRATVSGLKPGRYVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT 540  
Sbjct: 480 DKEMQSYSTLKVATTRATVSGLKPGRYVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT 539  
NOV2: 541 RTIVWICLTLITGLVVLRLICKKRHCGSKAFQDSDEEKMHYQNGQAPPPVFLPLHHP 600  
Sbjct: 540 RTIVWICLTLITGLVVLRLICKKRHCGSKAFQDSDEEKMHYQNGQAPPPVFLPLNHP 599  
NOV2: 601 PGKLPPEQFYAEPEHTYEEPGRAGRSFTREIEASRIHIEKIIIGSGDSGEVCYGRRLRVPGQR 660  
Sbjct: 600 PGKFPETQFSAEPEHTYEEPGRAGRSFTREIEASRIHIEKIIIGSGESGEVCYGRQLQVPGQR 659  
NOV2: 661 DVPVAIKALKAGYTERQRQDFLSEASIMQFDHPNIIRLEGVVTRGRRLAMIVTEYMEMGS 720  
Sbjct: 660 DVPVAIKALKAGYTERQRQDFLSEAAIMQFDHPNIIRLEGVVTRGRRLAMIVTEYMEMGS 719  
NOV2: 721 LDTFLRTHDGQFTIMQLVGMLRGVGAGMRYLSDLGYVHRDLAARNVLVDSNLVCKVSDFG 780  
Sbjct: 720 LDAFLRTHDGQFTIVQLVGMLRGVGAGMRYLSDLGYIHRDLAARNVLVDSNLVCKVSDFG 779  
NOV2: 781 LSRVLEDDPDAAYTTGGKIPIRWTAPEAIAFRFTSSASDVWSFGVVMWEVLAYERPYW 840  
Sbjct: 780 LSRALEDDPEAAYTTAGGKIPIRWTAPEAIAFRFTSSASDVWSFGVVMWEVLAYERPYW 839  
NOV2: 841 NMTNRDVISSEEGYRLPAPMCPHALHQLMLDCWHKDRAQRPRFSQIVSVDALIRSPE 900  
Sbjct: 840 NMTNQDVISSEEGYRLPAPMCPRALHQLMLDCWHKDRAQRPRFAHVVSVLDALVHSPE 899  
NOV2: 901 SLRATATVSRCPPPAFVRSCFDLRRGGSGGGGLTVGDWLDLSIRMGRYRDHFAAGGYSSLG 960  
Sbjct: 900 SLRATATVSRCPPPAFARSCFDLRRGGSGNGDLTVGDWLDLSIRMGRYRDHFAAGGYSSLG 959  
NOV2: 961 MVLRMNAQDVRALGITLMGHQKKILGSIQTMR 992 (SEQ ID NO:5)  
Sbjct: 960 MVLRMNAQDVRALGITLMGHQKKILGSIQTMR 991 (SEQ ID NO:52)

Table 6A beginning on page 14 has been amended as follows:

**Table 6A.**  
**Comparison between a NOV2 polypeptide and human ephrin receptor EphA8**

>ref|NP\_065387.1| EphA8; Ephrin receptor EphA8 (eph- and elk-related kinase); Hek3; eph-, elk-related tyrosine kinase; ephrin receptor EphA8  
emb|CAB81612.1| (AL035703) dJ61A9.1 (tyrosine kinase) [Homo sapiens]  
Length = 1005

Score = 2054 bits (5262), Expect = 0.0  
Identities = 992/992 (100%), Positives = 992/992 (100%)

NOV2 : 1 MAPARGRILPPALWVVTAAAAATCVSAARGEVNLLDTSTIHDGWLTYPAHGWDSINEV 60  
Sbjct: 1 MAPARGRILPPALWVVTAAAAATCVSAARGEVNLLDTSTIHDGWLTYPAHGWDSINEV 60  
NOV2 : 61 DESFQPIHTYQVCNVMSPNQNNWLRTSWVPRDGARRVYAEIKFTLRCNSMPGVLTCKE 120  
Sbjct: 61 DESFQPIHTYQVCNVMSPNQNNWLRTSWVPRDGARRVYAEIKFTLRCNSMPGVLTCKE 120

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NOV2 : 121 TPNLYYLESDRDLGASTQESQFLKIDTIAADESFTGADLGVRRLKLNTTEVRSGPLSKRG 180  
[TPNLYYLESDRDLGASTQESQFLKIDTIAADESFTGADLGVRRLKLNTTEVRSGPLSKRG]  
Sbjct: 121 TPNLYYLESDRDLGASTQESQFLKIDTIAADESFTGADLGVRRLKLNTTEVRSGPLSKRG 180

NOV2 : 181 FYLAFQDIGACLAILSLRIYYKKCPAMVRNLAAFSEAVTGADSSLVEVRGQCVRHSEER 240  
Sbjct: 181 FYLAFQDIGACLAILSLRIYYKKCPAMVRNLAAFSEAVTGADSSLVEVRGQCVRHSEER 240

NOV2 : 241 DTPKMYCSAEGEWLVPIGKCVCSAGYEERRDACPACELGFYKSAPGDQLCARCPHSHSA 300  
Sbjct: 241 DTPKMYCSAEGEWLVPIGKCVCSAGYEERRDACPACELGFYKSAPGDQLCARCPHSHSA 300

NOV2 : 301 APAAQACHCDLSYYRAALDPSSACTRPPSAPVNLISSVNGTSVTLEWAPPLDPGGRSDI 360  
[APAAQACHCDLSYYRAALDPSSACTRPPSAPVNLISSVNGTSVTLEWAPPLDPGGRSDI]  
Sbjct: 301 APAAQACHCDLSYYRAALDPSSACTRPPSAPVNLISSVNGTSVTLEWAPPLDPGGRSDI 360

NOV2 : 361 TYNAVCRRCPWALSRCACSGTRFVPPQTSLVQASLLVANLLAHMNYSFWIEAVNGVSD 420  
Sbjct: 361 TYNAVCRRCPWALSRCACSGTRFVPPQTSLVQASLLVANLLAHMNYSFWIEAVNGVSD 420

NOV2 : 421 LSPEPRRAAVVNITTNAQAPSQVVIRQERAGQTSVSLWQEPQPNGLILEYEIKYYEK 480  
Sbjct: 421 LSPEPRRAAVVNITTNAQAPSQVVIRQERAGQTSVSLWQEPQPNGLILEYEIKYYEK 480

NOV2 : 481 DKEMQSYSTLKAVTTRATVSGLKPGRTRYVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT 540  
[DKEMQSYSTLKAVTTRATVSGLKPGRTRYVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT]  
Sbjct: 481 DKEMQSYSTLKAVTTRATVSGLKPGRTRYVFQVRARTSAGCGRFSQAMEVETGKPRPRYDT 540

NOV2 : 541 RTIVWICLTLITGLVLLLLICKKRHCGSKAFQDSDEEKMHYQNGQAPPVFLPLHHP 600  
Sbjct: 541 RTIVWICLTLITGLVLLLLICKKRHCGSKAFQDSDEEKMHYQNGQAPPVFLPLHHP 600

NOV2 : 601 PGKLPEPQFYAEPTHYEEPGAGRGSFTREIEASRIHIEKIIGSGDSGEVCYGRLRPGQR 660  
Sbjct: 601 PGKLPEPQFYAEPTHYEEPGAGRGSFTREIEASRIHIEKIIGSGDSGEVCYGRLRPGQR 660

NOV2 : 661 DVPVAIKALKAGYTERQRDFLSEASIMQFDHPNIIRLEGVVTRGRRLAMIVTEYMENG 720  
Sbjct: 661 DVPVAIKALKAGYTERQRDFLSEASIMQFDHPNIIRLEGVVTRGRRLAMIVTEYMENG 720

NOV2 : 721 LDTFLRTHDGQFTIMQLVGMLRGVGAGMRYLSDLGIVHDLAARNVLVDSNLVCKVSDFG 780  
Sbjct: 721 LDTFLRTHDGQFTIMQLVGMLRGVGAGMRYLSDLGIVHDLAARNVLVDSNLVCKVSDFG 780

NOV2 : 781 LSRVLEDDPDAAYTTGGKIPRWTAPAEAIAFRFTSSASDVWSFGVVMWEVLAYGERPYW 840  
Sbjct: 781 LSRVLEDDPDAAYTTGGKIPRWTAPAEAIAFRFTSSASDVWSFGVVMWEVLAYGERPYW 840

NOV2 : 841 NMTNRDVISSVEEGYRLPAPMCPHALHQLMLDCWHKDRAQRPRFSQIVSVDALIRSPE 900  
Sbjct: 841 NMTNRDVISSVEEGYRLPAPMCPHALHQLMLDCWHKDRAQRPRFSQIVSVDALIRSPE 900

NOV2 : 901 SLRATATVSRCPPPAFVRSCFDLRGSGGGGGLTVDWLDSIRMGRYRDHFAAGGYSSLG 960  
Sbjct: 901 SLRATATVSRCPPPAFVRSCFDLRGSGGGGGLTVDWLDSIRMGRYRDHFAAGGYSSLG 960

NOV2 : 961 MVLRMNAQDVRALGITLMGHQKKILGSIQTMR 992 (SEQ ID NO:5)  
Sbjct: 961 MVLRMNAQDVRALGITLMGHQKKILGSIQTMR 992 (SEQ ID NO:53)

The paragraph beginning at line 4 in Table 7 on page 16 has been amended as follows:

Table 7 shows multiple sequence alignment of the NOV2 ephrin type-A receptor 8-like protein of the invention, shown as AL035703 Spliced2, with similar proteins. The various aligned proteins are as follows: AL035703 Spliced2 (SEQ ID NO:5) with several proteins: EPA8 Mouse (SEQ ID NO:54), EPA5 Human (SEQ ID NO:55) and EPA5 Chick (SEQ ID NO:56). (Black outlined amino acids indicate potential regions of conserved sequence; greyed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs)

The paragraph beginning at line 5 in Table 9 on page 20 has been amended as follows:

Table 9 shows sequence alignment between a NOV3 polypeptide with several members of the human fibronectin leucine repeat transmembrane family: AAF28461.1|AF169 (SEQ ID NO:57), AAF28460.1|AF169 (SEQ ID NO:58) and AAF28459.1|AF169 (SEQ ID NO:59).  
 (Black outlined amino acids indicate potential regions of conserved sequence; greyed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs)

Table 9, continued on page 21 has been amended as follows:

[TABLE 9. continued] TABLE 9A.

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>ref|NP_037412.1| fibronectin leucine rich transmembrane protein 1
  gb|AAF28459.1|AF169675_1 (AF169675) leucine-rich repeat transmembrane protein FLRT1
[Homo
          sapiens]
Length = 674

Score = 1365 bits (3494), Expect = 0.0
Identities = 673/674 (99%), Positives = 674/674 (99%)

NOV3:  1  MVVAHPTATATTPTATVTATVVMTTATMDLRDWLFLCYGLIAFLTEVIDSTTCPSVCRC 60
||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Sbjct: 1  MVVAHPTATATTPTATVTATVVMTTATMDLRDWLFLCYGLIAFLTEVIDSTTCPSVCRC 60

NOV3:  61  DNGFIYCNDRGLTSIPADIPDDATTLYLQNNQINNAGIPQDLKTKVNVQVIYLYENDLDE 120
||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Sbjct: 61  DNGFIYCNDRGLTSIPADIPDDATTLYLQNNQINNAGIPQDLKTKVNVQVIYLYENDLDE 120

NOV3:  121  FPINLPRSLRELHLQDNNVRTIARDSLARIPLLEKLHLDLNSVSTVSIEEDAFADSKQLK 180
||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Sbjct: 121  FPINLPRSLRELHLQDNNVRTIARDSLARIPLLEKLHLDLNSVSTVSIEEDAFADSKQLK 180

NOV3:  181  LLFLSRNHLSIIPSGLPHTLEELRLDDNRISTIPLHAFKGLNSLRLVLVDGNLLANQRIA 240
||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||

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Sbjct: 181 LLFLSRNLSSIPSGLPHTLEELRLDDNRISTIPLHAFKGLNSLRRILVLDGNLLANQRIA 240  
NOV3: 241 DDTFSRLQNLTELSLVRNSLAAPPLNLP SAHLQKLYLQDNAISHI PYNTLAKMRELERLD 300  
Sbjct: 241 DDTFSRLQNLTELSLVRNSLAAPPLNLP SAHLQKLYLQDNAISHI PYNTLAKMRELERLD 300  
NOV3: 301 LSNNNLTTLPRGLFDDLGNAQLLLRRNNPWFCGCNLMWLRDWVKARA AVNVRGGLMCQGP 360  
Sbjct: 301 LSNNNLTTLPRGLFDDLGNAQLLLRRNNPWFCGCNLMWLRDWVKARA AVNVRGGLMCQGP 360  
NOV3: 361 EKVRGMAIKDITSEMDEC FETGPQGGVANAAKTTASN HASATT PQGSLFTLAKRPGLR 420  
Sbjct: 361 EKVRGMAIKDITSEMDEC FETGPQGGVANAAKTTASN HASATT PQGSLFTLAKRPGLR 420  
NOV3: 421 LPDSNIDYPMATGDGAKTLAIHVKALTADSIRITWKATL PASSFRLSWLRLGHSPAVGSI 480  
Sbjct: 421 LPDSNIDYPMATGDGAKTLAIHVKALTADSIRITWKATL PASSFRLSWLRLGHSPAVGSI 480  
NOV3: 481 TETLVQGDKTEYLLTALEPKSTYIICMVTMETS NAYVADETPVCAKAETADS YGPTTTLN 540  
Sbjct: 481 TETLVQGDKTEYLLTALEPKSTYIICMVTMETS NAYVADETPVCAKAETADS YGPTTTLN 540  
NOV3: 541 QEQNAGPMA SLP LAGIIGGAVALVFLFLV LGAICWYVHQAGELLTRERAYNRGSRKDDY 600  
Sbjct: 541 QEQNAGPMA SLP LAGIIGGAVALVFLFLV LGAICWYVHQAGELLTRERAYNRGSREKDDY 600  
NOV3: 601 MESGTTK DNSILEIRGPGLQMLP INPYRAKEEYVVHTIFPSNGSSLCKATH TIGYGTTRG 660  
Sbjct: 601 MESGTTK DNSILEIRGPGLQMLP INPYRAKEEYVVHTIFPSNGSSLCKATH TIGYGTTRG 660  
NOV3: 661 YRDGGIPDIDYSYT 674 (SEQ ID NO:7)  
Sbjct: 661 YRDGGIPDIDYSYT 674 (SEQ ID NO:60)

The paragraph beginning at line 6 in Table 10 on page 22 has been amended as follows:

Table 10 shows sequence alignment between a NOV3 polypeptide with various fibromodulins: ACC NO: O43408 (SEQ ID NO:61), ACC NO: AP000597 (SEQ ID NO:7), ACC NO: O43155 (SEQ ID NO:62), ACC NO: O42235 (SEQ ID NO:63) and FMOD Bovin FM (SEQ ID NO:64). (Black outlined amino acids indicate potential regions of conserved sequence; greyed amino acids represent amino acids conservatively substituted; and non-highlighted amino acids indicate positions in which mutations to a broad range of alternative amino acid residues occurs)